



IFWO

RAW SEQUENCE LISTING

DATE: 08/23/2004

PATENT APPLICATION: US/10/676,873A

TIME: 11:15:35

Input Set : A:\COTH-P01-002.TXT

Output Set: N:\CRF4\08232004\J676873A.raw

ENTERED

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4 <110> APPLICANT: Chan, John
5       Baynes, Brian
6       Zhang, Shengsheng
8 <120> TITLE OF INVENTION: METHODS OF ENGINEERING SPATIALLY
9       CONSERVED MOTIFS IN POLYPEPTIDES
12 <130> FILE REFERENCE: COTH-P01-002
14 <140> CURRENT APPLICATION NUMBER: US 10/676,873A
15 <141> CURRENT FILING DATE: 2003-09-30
17 <150> PRIOR APPLICATION NUMBER: US 60/414,688
18 <151> PRIOR FILING DATE: 2002-09-30
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 474
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Nucleotide sequence of TNF alpha chain b mutation
31       b_tyr_119_asp
33 <400> SEQUENCE: 1
34 gtcagatcat cttctcgaac cccgagtgac aagcctgtag cccatgttgt agcaaaccct 60
35 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgcctcct ggccaatggc 120
36 gtggagctga gagataacca gctggtggtg ccatcagagg gcctgtacct catctactcc 180
37 caggtcctct tcaagggccca aggctgcccc tccaccatg tgctcctcac ccacaccatc 240
38 agccgcatcg ccgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300
39 tgccagaggg agaccccaga gggggctgag gccaaaccct ggtatgagcc catcgatctg 360
40 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgac 420
41 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga      474
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44 <211> LENGTH: 157
45 <212> TYPE: PRT
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Protein sequence of TNF alpha chain b mutation
50       b_tyr_119_asp
52 <400> SEQUENCE: 2
53 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala Gly Val
54 1      5      10      15
55 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
56      20      25      30
57 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
58      35      40      45
59 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe

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60      50      55      60
61 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
62 65      70      75      80
63 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
64      85      90      95
65 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
66      100      105      110
67 Pro Gln Tyr Glu Pro Ile Asp Leu Gly Gly Val Phe Gln Leu Glu Lys
68      115      120      125
69 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
70      130      135      140
71 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
72 145      150      155
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 474
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Nucleotide sequence of TNF alpha chain c mutations
82      c_tyr_119_his, c_tyr_59_ser
84 <400> SEQUENCE: 3
85 gtcagatcat cttctcgaac cccgagtgc aagcctgtag cccatgttgt agcaaaccct 60
86 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120
87 gtggagctga gagataacca gctggtggtg ccatcagagg gcctgtacct catcagttcc 180
88 caggtcctct tcaagggcca aggctgcccc tccacccatg tgctcctcac ccacaccatc 240
89 agccgcacgc ccgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300
90 tgccagaggg agaccccaga gggggctgag gccaaagccct ggtatgagcc catccatctg 360
91 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggccccgac 420
92 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga 474
94 <210> SEQ ID NO: 4
95 <211> LENGTH: 157
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Protein sequence of TNF alpha chain c mutations
101      c_tyr_119_his, c_tyr_59_ser
103 <400> SEQUENCE: 4
104 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
105 1      5      10      15
106 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
107      20      25      30
108 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
109      35      40      45
110 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Ser Ser Gln Val Leu Phe
111      50      55      60
112 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
113 65      70      75      80
114 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
115      85      90      95

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116 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
117           100           105           110
118 Pro Gln Tyr Glu Pro Ile His Leu Gly Gly Val Phe Gln Leu Glu Lys
119           115           120           125
120 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
121           130           135           140
122 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
123 145           150           155
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VERIFICATION SUMMARY

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